

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NI, JIAN
FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
- (ii) TITLE OF INVENTION: HUMAN IRAK-2
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
(B) STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
(C) CITY: WASHINGTON
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: STEFFE, ERIC K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1806 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 34..1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGGCGCGC CGGAGCCGGC CCCGTAGCGT GCC ATG GCC TGC TAC ATC TAC CAG
Met Ala Cys Tyr Ile Tyr Gln
1 5

54

CTG Leu	CCC Pro	TCC Ser 10	TGG Trp	GTG Val	CTG Leu	GAC Asp 15	GAC Asp 15	CTG Leu	TGC Cys	CGC Arg	AAC Asn 20	ATG Met 20	GAC Asp	GCG Ala	CTC Leu	102
AGC Ser	GAG Glu 25	TGG Trp	GAC Asp	TGG Trp	ATG Met 30	GAG Glu 30	TTC Phe	GCC Ala	TCC Ser	TAC Tyr	GTG Val 35	ATC Ile	ACA Thr	GAC Asp	CTG Leu	150
ACC Thr 40	CAG Gln	CTG Leu	CGG Arg	AAG Lys	ATC Ile 45	AAG Lys	TCC Ser	ATG Met	GAG Glu	CGG Arg 50	GTG Val	CAG Gln	GGT Gly	GTG Val	AGC Ser 55	198
ATC Ile	ACG Thr	CGG Arg	GAG Glu	CTG Leu 60	CTG Leu	TGG Trp	TGG Trp	TGG Trp	GGC Gly 65	ATG Met	CGG Arg	CAG Gln	GCC Ala	ACC Thr 70	GTC Val	246
CAG Gln	CAA Gln	CTT Leu	GTG Val 75	GAC Asp	CTC Leu	CTG Leu	TGC Cys 80	CGC Arg 80	CTG Leu	GAG Glu	CTC Leu	TAC Tyr	CGG Arg 85	GCT Ala	GCC Ala	294
CAG Gln	ATC Ile	ATC Ile 90	CTG Leu	AAC Asn	TGG Trp	AAA Lys	CCG Pro 95	GCT Ala	CCT Pro	GAA Glu	ATC Ile	AGG Arg 100	TGT Cys	CCC Pro	ATT Ile	342
CCA Pro	GCC Ala 105	TTC Phe	CCT Pro	GAC Asp	TCT Ser	GTG Val 110	AAG Lys	CCA Pro	GAA Glu	AAG Lys	CCT Pro 115	TTG Leu	GCA Ala	GCT Ala	TCT Ser	390
GTA Val 120	AGA Arg	AAG Lys	GCT Ala	GAG Glu	GAT Asp 125	GAA Glu	CAG Gln	GAA Glu	GAG Glu	GGG Gly 130	CAG Gln	CCT Pro	GTG Val	AGG Arg	ATG Met 135	438
GCC Ala	ACC Thr	TTT Phe	CCA Pro	GGC Gly 140	CCA Pro	GGG Gly	TCC Ser	TCT Ser	CCA Pro 145	GCC Ala	AGA Arg	GCC Ala	CAC His	CAG Gln 150	CCG Pro	486
GCC Ala	TTT Phe	CTC Leu	CAG Gln 155	CCT Pro	CCT Pro	GAA Glu	GAA Glu	GAT Asp 160	GCC Ala	CCT Pro	CAT His	TCC Ser	TTG Leu 165	AGA Arg	AGC Ser	534
GAC Asp	CTC Leu	CCC Pro 170	ACT Thr	TCG Ser	TCT Ser	GAT Asp	TCA Ser 175	AAG Lys	GAC Asp	TTC Phe	AGC Ser	ACC Thr 180	TCC Ser	ATT Ile	CCT Pro	582
AAG Lys	CAG Gln 185	GAA Glu	AAA Lys	CTT Leu	TTG Leu	AGC Ser 190	TTG Leu	GCT Ala	GGA Gly	GAC Asp 195	AGC Ser 195	CTT Leu	TTC Phe	TGG Trp	AGT Ser	630
GAG Glu 200	GCA Ala	GAC Asp	GTG Val	GTC Val	CAG Gln 205	GCA Ala	ACC Thr	GAT Asp	GAC Asp	TTC Phe 210	AAT Asn	CAA Gln	AAC Asn	CGC Arg	AAA Lys 215	678
ATC Ile	AGC Ser	CAG Gln	GGG Gly	ACC Thr 220	TTT Phe	GCT Ala	GAC Asp	GTC Val	TAC Tyr 225	AGA Arg	GGG Gly	CAC His	AGG Arg	CAC His 230	GGG Gly	726
AAG Lys	CCA Pro	TTC Phe 235	GTC Val	TTC Phe	AAG Lys	AAG Lys	CTC Leu 240	AGA Arg	GAG Glu	ACA Thr	GCC Ala	TGT Cys 245	TCA Ser	AGT Ser	CCA Pro	774
GGA Gly	TCA Ser	ATC Ile 250	GAA Glu	AGA Arg	TTC Phe	TTC Phe	CAG Gln 255	GCA Ala	GAG Glu	TTG Leu	CAG Gln	ATT Ile 260	TGT Cys	CTT Leu	AGA Arg	822

TGC Cys 265	TGC Cys	CAC His	CCC Pro	AAT Asn	GTC Val	TTA Leu 270	CCT Pro	GTG Val	CTG Leu	GGC Gly	TTC Phe 275	TGT Cys	GCT Ala	GCA Ala	AGA Arg	870
CAG Gln 280	TTT Phe	CAC His	AGC Ser	TTC Phe	ATC Ile 285	TAC Tyr	CCC Pro	TAC Tyr	ATG Met	GCA Ala 290	AAT Asn	GGT Gly	TCC Ser	CTA Leu	CAG Gln 295	918
GAC Asp	AGA Arg	CTG Leu	CAG Gln	GGT Gly 300	CAG Gln	GGT Gly	GGC Gly	TCG Ser	GAA Glu 305	CCC Pro	CTC Leu	CCC Pro	TGG Trp	CCC Pro 310	CAG Gln	966
CGT Arg	GTC Val	AGC Ser	ATC Ile 315	TGC Cys	TCA Ser	GGG Gly	CTG Leu 320	CTC Leu	TGT Cys	GCC Ala	GTC Val	GAG Glu	TAC Tyr 325	CTG Leu	CAT His	1014
GGT Gly	CTG Leu	GAG Glu 330	ATC Ile	ATC Ile	CAC His	AGC Ser	AAC Asn 335	GTC Val	AAG Lys	AGC Ser	TCT Ser	AAT Asn 340	GTC Val	TTG Leu	CTG Leu	1062
GAC Asp 345	CAA Gln	AAT Asn	CTC Leu	ACC Thr	CCC Pro	AAA Lys 350	CTT Leu	GCT Ala	CAC His	CCA Pro	ATG Met 355	GCT Ala	CAT His	CTG Leu	TGT Cys	1110
CCT Pro 360	GTC Val	AAC Asn	AAA Lys	AGG Arg	TCA Ser 365	AAA Lys	TAC Tyr	ACC Thr	ATG Met	ATG Met 370	AAG Lys	ACT Thr	CAC His	CTG Leu	CTC Leu 375	1158
CGG Arg	ACG Thr	TCA Ser	GCC Ala	GCG Ala 380	TAT Tyr	CTG Leu	CCA Pro	GAG Glu	GAT Asp 385	TTC Phe	ATC Ile	CGG Arg	GTG Val	GGG Gly 390	CAG Gln	1206
CTG Leu	ACA Thr	AAG Lys	CGA Arg 395	GTG Val	GAC Asp	ATC Ile	TTC Phe	AGC Ser 400	TGT Cys	GGA Gly	ATA Ile	GTG Val	TTG Leu 405	GCC Ala	GAG Glu	1254
GTC Val	CTC Leu 410	ACG Thr	GGC Gly	ATC Ile	CCT Pro	GCA Ala	ATG Met 415	GAT Asp	AAC Asn	AAC Asn	CGA Arg	AGC Ser 420	CCG Pro	GTT Val	TAC Tyr	1302
CTG Leu 425	AAG Lys	GAC Asp	TTA Leu	CTC Leu	CTC Leu	AGT Ser 430	GAA Glu	ATT Ile	CCA Pro	AGC Ser	AGC Ser 435	ACC Thr	GCC Ala	TCG Ser	CTC Leu	1350
TGC Cys 440	TCC Ser	AGG Arg	AAG Lys	ACG Thr	GGC Gly 445	GTG Val	GAG Glu	AAC Asn	GTG Val	ATG Met 450	GCA Ala	AAG Lys	GAG Glu	ATC Ile	TGC Cys 455	1398
CAG Gln	AAG Lys	TAC Tyr	CTG Leu	GAG Glu 460	AAG Lys	GGC Gly	GCA Ala	GGG Gly	AGG Arg 465	CTT Leu	CCG Pro	GAG Glu	GAC Asp	TGC Cys 470	GCC Ala	1446
GAG Glu	GCC Ala	CTG Leu	GCC Ala	ACG Thr 475	GCT Ala	GCC Ala	TGC Cys	CTG Leu 480	TGC Cys	CTG Leu	CGG Arg	AGG Arg	CGT Arg 485	AAC Asn	ACC Thr	1494
AGC Ser	CTG Leu 490	CAG Gln	GAG Glu	GTG Val	TGT Cys	GGC Gly	TCT Ser 495	GTG Val	GCT Ala	GCT Ala	GTG Val	GAA Glu 500	GAG Glu	CGG Arg	CTC Leu	1542
CGA Arg 505	GGT Gly	CGG Arg	GAG Glu	ACG Thr	TTG Leu	CTC Leu 510	CCT Pro	TGG Trp	AGT Ser	GGG Gly	CTT Leu 515	TCT Ser	GAG Glu	GGT Gly	ACA Thr	1590

GGC TCT TCT TCC AAC ACC CCA GAG GAA ACA GAC GAC GTT GAC AAT TCC	1638
Gly Ser Ser Ser Asn Thr Pro Glu Glu Thr Asp Asp Val Asp Asn Ser	
520 525 530 535	
AGC CTT GAT GCC TCC TCC TCC ATG AGT GTG GCA CCC TGG GCA GGG GCT	1686
Ser Leu Asp Ala Ser Ser Ser Met Ser Val Ala Pro Trp Ala Gly Ala	
540 545 550	
GCC ACC CCA CTT CTC CCC ACA GAG AAT GGG GAA GGA AGG CTG CGG GTC	1734
Ala Thr Pro Leu Leu Pro Thr Glu Asn Gly Glu Gly Arg Leu Arg Val	
555 560 565	
ATC GTG GGA AGG GAG GCT GAC TCC TCC TCT GAG GCC TGT GTT GGC CTG	1782
Ile Val Gly Arg Glu Ala Asp Ser Ser Ser Glu Ala Cys Val Gly Leu	
570 575 580	
GAG CCT CCC CAG GAT GTT ACA TAA	1806
Glu Pro Pro Gln Asp Val Thr	
585 590	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 590 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Cys Tyr Ile Tyr Gln Leu Pro Ser Trp Val Leu Asp Asp Leu	
1 5 10 15	
Cys Arg Asn Met Asp Ala Leu Ser Glu Trp Asp Trp Met Glu Phe Ala	
20 25 30	
Ser Tyr Val Ile Thr Asp Leu Thr Gln Leu Arg Lys Ile Lys Ser Met	
35 40 45	
Glu Arg Val Gln Gly Val Ser Ile Thr Arg Glu Leu Leu Trp Trp Trp	
50 55 60	
Gly Met Arg Gln Ala Thr Val Gln Gln Leu Val Asp Leu Leu Cys Arg	
65 70 75 80	
Leu Glu Leu Tyr Arg Ala Ala Gln Ile Ile Leu Asn Trp Lys Pro Ala	
85 90 95	
Pro Glu Ile Arg Cys Pro Ile Pro Ala Phe Pro Asp Ser Val Lys Pro	
100 105 110	
Glu Lys Pro Leu Ala Ala Ser Val Arg Lys Ala Glu Asp Glu Gln Glu	
115 120 125	
Glu Gly Gln Pro Val Arg Met Ala Thr Phe Pro Gly Pro Gly Ser Ser	
130 135 140	
Pro Ala Arg Ala His Gln Pro Ala Phe Leu Gln Pro Pro Glu Glu Asp	
145 150 155 160	
Ala Pro His Ser Leu Arg Ser Asp Leu Pro Thr Ser Ser Asp Ser Lys	

165					170					175					
Asp	Phe	Ser	Thr	Ser	Ile	Pro	Lys	Gln	Glu	Lys	Leu	Leu	Ser	Leu	Ala
			180					185					190		
Gly	Asp	Ser	Leu	Phe	Trp	Ser	Glu	Ala	Asp	Val	Val	Gln	Ala	Thr	Asp
		195					200					205			
Asp	Phe	Asn	Gln	Asn	Arg	Lys	Ile	Ser	Gln	Gly	Thr	Phe	Ala	Asp	Val
		210				215					220				
Tyr	Arg	Gly	His	Arg	His	Gly	Lys	Pro	Phe	Val	Phe	Lys	Lys	Leu	Arg
225					230					235					240
Glu	Thr	Ala	Cys	Ser	Ser	Pro	Gly	Ser	Ile	Glu	Arg	Phe	Phe	Gln	Ala
				245					250					255	
Glu	Leu	Gln	Ile	Cys	Leu	Arg	Cys	Cys	His	Pro	Asn	Val	Leu	Pro	Val
			260					265					270		
Leu	Gly	Phe	Cys	Ala	Ala	Arg	Gln	Phe	His	Ser	Phe	Ile	Tyr	Pro	Tyr
		275					280					285			
Met	Ala	Asn	Gly	Ser	Leu	Gln	Asp	Arg	Leu	Gln	Gly	Gln	Gly	Gly	Ser
	290					295					300				
Glu	Pro	Leu	Pro	Trp	Pro	Gln	Arg	Val	Ser	Ile	Cys	Ser	Gly	Leu	Leu
305					310					315					320
Cys	Ala	Val	Glu	Tyr	Leu	His	Gly	Leu	Glu	Ile	Ile	His	Ser	Asn	Val
				325					330					335	
Lys	Ser	Ser	Asn	Val	Leu	Leu	Asp	Gln	Asn	Leu	Thr	Pro	Lys	Leu	Ala
			340					345					350		
His	Pro	Met	Ala	His	Leu	Cys	Pro	Val	Asn	Lys	Arg	Ser	Lys	Tyr	Thr
		355					360					365			
Met	Met	Lys	Thr	His	Leu	Leu	Arg	Thr	Ser	Ala	Ala	Tyr	Leu	Pro	Glu
	370					375					380				
Asp	Phe	Ile	Arg	Val	Gly	Gln	Leu	Thr	Lys	Arg	Val	Asp	Ile	Phe	Ser
385					390					395					400
Cys	Gly	Ile	Val	Leu	Ala	Glu	Val	Leu	Thr	Gly	Ile	Pro	Ala	Met	Asp
				405					410					415	
Asn	Asn	Arg	Ser	Pro	Val	Tyr	Leu	Lys	Asp	Leu	Leu	Leu	Ser	Glu	Ile
			420					425					430		
Pro	Ser	Ser	Thr	Ala	Ser	Leu	Cys	Ser	Arg	Lys	Thr	Gly	Val	Glu	Asn
		435					440					445			
Val	Met	Ala	Lys	Glu	Ile	Cys	Gln	Lys	Tyr	Leu	Glu	Lys	Gly	Ala	Gly
	450					455					460				
Arg	Leu	Pro	Glu	Asp	Cys	Ala	Glu	Ala	Leu	Ala	Thr	Ala	Ala	Cys	Leu
465					470					475					480
Cys	Leu	Arg	Arg	Arg	Asn	Thr	Ser	Leu	Gln	Glu	Val	Cys	Gly	Ser	Val
				485					490					495	
Ala	Ala	Val	Glu	Glu	Arg	Leu	Arg	Gly	Arg	Glu	Thr	Leu	Leu	Pro	Trp
			500					505					510		

Ser Gly Leu Ser Glu Gly Thr Gly Ser Ser Ser Asn Thr Pro Glu Glu
515 520 525

Thr Asp Asp Val Asp Asn Ser Ser Leu Asp Ala Ser Ser Ser Met Ser
530 535 540

Val Ala Pro Trp Ala Gly Ala Ala Thr Pro Leu Leu Pro Thr Glu Asn
545 550 555 560

Gly Glu Gly Arg Leu Arg Val Ile Val Gly Arg Glu Ala Asp Ser Ser
565 570 575

Ser Glu Ala Cys Val Gly Leu Glu Pro Pro Gln Asp Val Thr
580 585 590

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 34..1908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGGCGCGC CGGAGCCGGC CCCGTAGCGT GCC ATG GCC TGC TAC ATC TAC CAG	54
Met Ala Cys Tyr Ile Tyr Gln	
1 5	
CTG CCC TCC TGG GTG CTG GAC GAC CTG TGC CGC AAC ATG GAC GCG CTC	102
Leu Pro Ser Trp Val Leu Asp Asp Leu Cys Arg Asn Met Asp Ala Leu	
10 15 20	
AGC GAG TGG GAC TGG ATG GAG TTC GCC TCC TAC GTG ATC ACA GAC CTG	150
Ser Glu Trp Asp Trp Met Glu Phe Ala Ser Tyr Val Ile Thr Asp Leu	
25 30 35	
ACC CAG CTG CGG AAG ATC AAG TCC ATG GAG CGG GTG CAG GGT GTG AGC	198
Thr Gln Leu Arg Lys Ile Lys Ser Met Glu Arg Val Gln Gly Val Ser	
40 45 50 55	
ATC ACG CGG GAG CTG CTG TGG TGG TGG GGC ATG CGG CAG GCC ACC GTC	246
Ile Thr Arg Glu Leu Leu Trp Trp Trp Gly Met Arg Gln Ala Thr Val	
60 65 70	
CAG CAA CTT GTG GAC CTC CTG TGC CGC CTG GAG CTC TAC CGG GCT GCC	294
Gln Gln Leu Val Asp Leu Leu Cys Arg Leu Glu Leu Tyr Arg Ala Ala	
75 80 85	
CAG ATC ATC CTG AAC TGG AAA CCG GCT CCT GAA ATC AGG TGT CCC ATT	342
Gln Ile Ile Leu Asn Trp Lys Pro Ala Pro Glu Ile Arg Cys Pro Ile	
90 95 100	
CCA GCC TTC CCT GAC TCT GTG AAG CCA GAA AAG CCT TTG GCA GCT TCT	390

Pro 105	Ala	Phe	Pro	Asp	Ser	Val 110	Lys	Pro	Glu	Lys	Pro 115	Leu	Ala	Ala	Ser	
GTA Val 120	AGA Arg	AAG Lys	GCT Ala	GAG Glu	GAT Asp 125	GAA Glu	CAG Gln	GAA Glu	GAG Glu	GGG Gly 130	CAG Gln	CCT Pro	GTG Val	AGG Arg	ATG Met 135	438
GCC Ala	ACC Thr	TTT Phe	CCA Pro	GGC Gly 140	CCA Pro	GGG Gly	TCC Ser	TCT Ser	CCA Pro 145	GCC Ala	AGA Arg	GCC Ala	CAC His	CAG Gln 150	CCG Pro	486
GCC Ala	TTT Phe	CTC Leu	CAG Gln 155	CCT Pro	CCT Pro	GAA Glu	GAA Glu	GAT Asp 160	GCC Ala	CCT Pro	CAT His	TCC Ser	TTG Leu 165	AGA Arg	AGC Ser	534
GAC Asp	CTC Leu	CCC Pro 170	ACT Thr	TCG Ser	TCT Ser	GAT Asp	TCA Ser 175	AAG Lys	GAC Asp	TTC Phe	AGC Ser	ACC Thr 180	TCC Ser	ATT Ile	CCT Pro	582
AAG Lys 185	CAG Gln	GAA Glu	AAA Lys	CTT Leu	TTG Leu	AGC Ser 190	TTG Leu	GCT Ala	GGA Gly	GAC Asp 195	AGC Ser	CTT Leu	TTC Phe	TGG Trp	AGT Ser	630
GAG Glu 200	GCA Ala	GAC Asp	GTG Val	GTC Val	CAG Gln 205	GCA Ala	ACC Thr	GAT Asp	GAC Asp 210	TTC Phe	AAT Asn	CAA Gln	AAC Asn	CGC Arg	AAA Lys 215	678
ATC Ile	AGC Ser	CAG Gln	GGG Gly	ACC Thr 220	TTT Phe	GCT Ala	GAC Asp	GTC Val	TAC Tyr 225	AGA Arg	GGG Gly	CAC His	AGG Arg	CAC His 230	GGG Gly	726
AAG Lys	CCA Pro	TTC Phe 235	GTC Val	TTC Phe	AAG Lys	AAG Lys	CTC Leu 240	AGA Arg	GAG Glu	ACA Thr	GCC Ala	TGT Cys 245	TCA Ser	AGT Ser	CCA Pro	774
GGA Gly	TCA Ser	ATC Ile 250	GAA Glu	AGA Arg	TTC Phe	TTC Phe	CAG Gln 255	GCA Ala	GAG Glu	TTG Leu	CAG Gln	ATT Ile 260	TGT Cys	CTT Leu	AGA Arg	822
TGC Cys 265	TGC Cys	CAC His	CCC Pro	AAT Asn	GTC Val	TTA Leu 270	CCT Pro	GTG Val	CTG Leu	GGC Gly 275	TTC Phe	TGT Cys	GCT Ala	GCA Ala	AGA Arg	870
CAG Gln 280	TTT Phe	CAC His	AGC Ser	TTC Phe	ATC Ile 285	TAC Tyr	CCC Pro	TAC Tyr	ATG Met	GCA Ala 290	AAT Asn	GGT Gly	TCC Ser	CTA Leu	CAG Gln 295	918
GAC Asp	AGA Arg	CTG Leu	CAG Gln	GGT Gly 300	CAG Gln	GGT Gly	GGC Gly	TCG Ser	GAC Asp 305	CCC Pro	CTC Leu	CCC Pro	TGG Trp	CCC Pro 310	CAG Gln	966
CGT Arg	GTC Val	AGC Ser	ATC Ile 315	TGC Cys	TCA Ser	GGG Gly	CTG Leu	CTC Leu 320	TGT Cys	GCC Ala	GTC Val	GAG Glu	TAC Tyr 325	CTG Leu	CAT His	1014
GGT Gly	CTG Leu	GAG Glu 330	ATC Ile	ATC Ile	CAC His	AGC Ser	AAC Asn 335	GTC Val	AAG Lys	AGC Ser	TCT Ser	AAT Asn 340	GTC Val	TTG Leu	CTG Leu	1062
GAC Asp 345	CAA Gln	AAT Asn	CTC Leu	ACC Thr	CCC Pro	AAA Lys 350	CTT Leu	GCT Ala	CAC His	CCA Pro	ATG Met 355	GCT Ala	CAT His	CTG Leu	TGT Cys	1110
CCT GTC	AAC	AAA	AGG	TCA	AAA	TAC	ACC	ATG	ATG	AAG	ACT	CAC	CTG	CTC		1158

Pro 360	Val	Asn	Lys	Arg	Ser 365	Lys	Tyr	Thr	Met	Met 370	Lys	Thr	His	Leu	Leu 375	
CGG Arg	ACG Thr	TCA Ser	GCC Ala	GCG Ala 380	TAT Tyr	CTG Leu	CCA Pro	GAG Glu	GAT Asp 385	TTC Phe	ATC Ile	CGG Arg	GTG Val	GGG Gly 390	CAG Gln	1206
GTG Val	ACA Thr	AAG Lys	CGA Arg 395	GTG Val	GAC Asp	ATC Ile	TTC Phe	AGC Ser 400	TGT Cys	GGA Gly	ATA Ile	GTG Val	TTG Leu 405	GCC Ala	GAG Glu	1254
GTC Val	CTC Leu	ACG Thr 410	GGC Gly	ATC Ile	CCT Pro	GCA Ala	ATG Met 415	GAT Asp	AAC Asn	AAC Asn	CGA Arg	AGC Ser 420	CCG Pro	GTT Val	TAC Tyr	1302
CTG Leu	AAG Lys 425	GAC Asp	TTA Leu	CTC Leu	CTC Leu	AGT Ser 430	GAA Glu	ATT Ile	CCA Pro	AGC Ser 435	AGC Ser	ACC Thr	GCC Ala	TCG Ser	CTC Leu	1350
TGC Cys 440	TCC Ser	AGG Arg	AAG Lys	ACG Thr	GGC Gly 445	GTG Val	GAG Glu	AAC Asn	GTG Val	ATG Met 450	GCA Ala	AAG Lys	GAG Glu	ATC Ile	TGC Cys 455	1398
CAG Gln	AAG Lys	TAC Tyr	CTG Leu	GAG Glu 460	AAG Lys	GGC Gly	GCA Ala	GGG Gly	AGG Arg 465	CTT Leu	CCG Pro	GAG Glu	GAC Asp	TGC Cys 470	GCC Ala	1446
GAG Glu	GCC Ala	CTG Leu	GCC Ala 475	ACG Thr	GCT Ala	GCC Ala	TGC Cys	CTG Leu 480	TGC Cys	CTG Leu	CGG Arg	AGG Arg	CGT Arg 485	AAC Asn	ACC Thr	1494
AGC Ser	CTG Leu	CAG Gln 490	GAG Glu	GTG Val	TGT Cys	GGC Gly	TCT Ser 495	GTG Val	GCT Ala	GCT Ala	GTG Val	GAA Glu 500	GAG Glu	CGG Arg	CTC Leu	1542
CGA Arg	GGT Gly 505	CGG Arg	GAG Glu	ACG Thr	TTG Leu	CTC Leu 510	CCT Pro	TGG Trp	AGT Ser	GGG Gly	CTT Leu 515	TCT Ser	GAG Glu	GGT Gly	ACA Thr	1590
GGC Gly 520	TCT Ser	TCT Ser	TCC Ser	AAC Asn	ACC Thr 525	CCA Pro	GAG Glu	GAA Glu	ACA Thr	GAC Asp 530	GAC Asp	GTT Val	GAC Asp	AAT Asn	TCC Ser 535	1638
AGC Ser	CTT Leu	GAT Asp	GCC Ala	TCC Ser 540	TCC Ser	TCC Ser	ATG Met	AGT Ser	GTG Val 545	GCA Ala	CCC Pro	TGG Trp	GCA Ala	GGG Gly 550	GCT Ala	1686
GCC Ala	ACC Thr	CCA Pro	CTT Leu 555	CTC Leu	CCC Pro	ACA Thr	GAG Glu	AAT Asn 560	GGG Gly	GAA Glu	GGA Gly	AGG Arg	CTG Leu 565	CGG Arg	GTC Val	1734
ATC Ile	GTG Val 570	GGA Gly	AGG Arg	GAG Glu	GCT Ala	GAC Asp	TCC Ser 575	TCC Ser	TCT Ser	GAG Glu	GCC Ala	TGT Cys 580	GTT Val	GGC Gly	CTG Leu	1782
GAG Glu	CCT Pro 585	CCC Pro	CAG Gln	GAT Asp	GTT Val	ACA Thr 590	GAA Glu	ACT Thr	TCG Ser	TGG Trp	CAA Gln 595	ATT Ile	GAG Glu	ATC Ile	AAT Asn	1830
GAG Glu 610	GCC Ala	AAA Lys	AGG Arg	AAA Lys	CTG Leu 605	ATG Met	GAG Glu	AAT Asn	ATT Ile	CTG Leu 610	CTC Leu	TAC Tyr	AAA Lys	GAG Glu	GAA Glu 615	1878
AAA	GTG	GAC	AGC	ATT	GAG	CTC	TTT	GGC	CCC	TGATGACCGG	AACACAGCTG					1928

Lys	Val	Asp	Ser	Ile	Glu	Leu	Phe	Gly	Pro	
				620					625	
AGGACCCTTG	TCCTCAGTTG	GAAAGATGAG	CATCAGATCA	AGAAAAAGGT	CTGAGGCAGA					1988
ATCCAAGATC	TGCCAGGAAA	CACACAACAA	AACATCTGCT	GTCCTGGGTG	GGAGGGAAAC					2048
TTCATTTTAC	TGGAATGAGT	TGGGAGAGAA	AGGCCCTCAG	CTTTTAGAGA	CACAAAAATC					2108
CATGAAGTCT	CTTCCTTTCT	GGGCTTTGTT	AGTCAGAGCA	GGGGATCAGA	GGAGACTGAA					2168
GCAGAAACCC	TGCACACGGG	CCCAGGATGT	GGCTGATTTT	GTGGTTCCGG	GGAGTATGTG					2228
ATGATAATCA	CCCCCAGCAG	ATTCCATTAC	CTCAGCAGCT	CTTGTTCCCC	CGCCACTGGC					2288
AGTTCGTCAA	TGCCATAGCA	TTTTCCAGAG	CTAAGATCTC	TGGGTTGTAT	TTGCTGACAG					2348
CCTGCAAGCT	TGCATGCTCT	GAAAGATTTT	TTTAGTTTTT	AATTTTTTTG	TAAAAATGGG					2408
GTCTCGCTTT	GTTGGCGCAA	TCCTCCCACC	TCAGACTCCC	AAAGTGCTGG	AATTACATTG					2468
GGAACCACTG	TGCCTGGCCT	GGAAACTTC	CAACTTGTGT	TCTCAGTGCA	GTTCTGACTC					2528
ACCTCTCTGG	GCCTCAGGTT	CTACAAATGC	CAGACACCTA	GCGAAGAGCT	CTGCAGGCTT					2588
TCCACTGCCT	GTATTGGAAG	TCTTGCAATT	CACATAATTA	TTCAGTCACT	GCCTGGTACC					2648
TTTATCTTCC	CATCCCATTA	ATGTTAGTGT	TTTTTAATGG	AGCTTTTATT	CTGAGAATAT					2708
GTGTTTCGTCT	GTTTGTGTTG	TTTTTGAGAC	AGAGTCTCAC	TTTGTCACCC	AGGCTGGAGT					2768
GCAGTGGCAC	GATCTCAGCT	CACTGCAAGC	TGTGCCTCTC	AGGTTTCAAG	TGATTCTCCT					2828
GCCTCAGCCT	CCTGAGTAGA	TGGGACTGTA	GGCACCTGCC	ACTATGCCTG	GCTAATTTTT					2888
GTGTTTTTAG	TAGAGACAGG	GTTTCACCAT	ATTGGCCAGG	CTGGTCTCGA	ACTACTGACC					2948
TCGTGATCTG	CCCGCCTTGG	CCTATCAAAG	TGTTGGGATT	ACAGGCTTGA	GCCACCGCAC					3008
CCGGCCGAGA	ATATGTGTTG	TTATTTATGA	CTGGATTATG	AAGAATCAGG	AGAATGCATT					3068
TCATGTCTGA	TTCTGCTGCT	AATTAAGTCA	ATCATTTAAT	TTTTGGGACC	TCAGTTTCTT					3128
TGTAAGTAAA	ATAACACCTG	CTTGTTCTTC	ATCCCTGGGC	TGTTGGGAGG	AACAGATGAG					3188
ACAGTGGCTA	TAGAAGCACT	TGGAAAATGC	ACTTGTCTCT	TTTTGTAAAA	TAAAAAGGTA					3248
TTAAATGTGT	ATTTCTGCCA	TGTACCTAAT	GATTATTCAG	TGCGTATATA	TCTGAAAAGT					3308
CATGTTGCAA	ATCTTTCTGT	GAAACAGATG	CTATTTTAAA	TTCACCTGGG	GAAATATCCT					3368
ATTTAAAGTA	ATCTATAGTA	ATTTCTTTTT	ATATAATAAA	AATATATTTG	TAAAGTCGAA					3428
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	A							3459

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 625 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Cys	Tyr	Ile	Tyr	Gln	Leu	Pro	Ser	Trp	Val	Leu	Asp	Asp	Leu
1				5					10					15	
Cys	Arg	Asn	Met	Asp	Ala	Leu	Ser	Glu	Trp	Asp	Trp	Met	Glu	Phe	Ala
			20					25					30		
Ser	Tyr	Val	Ile	Thr	Asp	Leu	Thr	Gln	Leu	Arg	Lys	Ile	Lys	Ser	Met
		35					40					45			
Glu	Arg	Val	Gln	Gly	Val	Ser	Ile	Thr	Arg	Glu	Leu	Leu	Trp	Trp	Trp
	50					55					60				
Gly	Met	Arg	Gln	Ala	Thr	Val	Gln	Gln	Leu	Val	Asp	Leu	Leu	Cys	Arg
65					70					75					80
Leu	Glu	Leu	Tyr	Arg	Ala	Ala	Gln	Ile	Ile	Leu	Asn	Trp	Lys	Pro	Ala
				85					90					95	
Pro	Glu	Ile	Arg	Cys	Pro	Ile	Pro	Ala	Phe	Pro	Asp	Ser	Val	Lys	Pro
			100					105					110		
Glu	Lys	Pro	Leu	Ala	Ala	Ser	Val	Arg	Lys	Ala	Glu	Asp	Glu	Gln	Glu
	115						120					125			
Glu	Gly	Gln	Pro	Val	Arg	Met	Ala	Thr	Phe	Pro	Gly	Pro	Gly	Ser	Ser
130						135					140				
Pro	Ala	Arg	Ala	His	Gln	Pro	Ala	Phe	Leu	Gln	Pro	Pro	Glu	Glu	Asp
145					150					155					160
Ala	Pro	His	Ser	Leu	Arg	Ser	Asp	Leu	Pro	Thr	Ser	Ser	Asp	Ser	Lys
				165					170					175	
Asp	Phe	Ser	Thr	Ser	Ile	Pro	Lys	Gln	Glu	Lys	Leu	Leu	Ser	Leu	Ala
			180					185					190		
Gly	Asp	Ser	Leu	Phe	Trp	Ser	Glu	Ala	Asp	Val	Val	Gln	Ala	Thr	Asp
	195						200					205			
Asp	Phe	Asn	Gln	Asn	Arg	Lys	Ile	Ser	Gln	Gly	Thr	Phe	Ala	Asp	Val
210						215					220				
Tyr	Arg	Gly	His	Arg	His	Gly	Lys	Pro	Phe	Val	Phe	Lys	Lys	Leu	Arg
225					230					235					240
Glu	Thr	Ala	Cys	Ser	Ser	Pro	Gly	Ser	Ile	Glu	Arg	Phe	Phe	Gln	Ala
				245					250					255	
Glu	Leu	Gln	Ile	Cys	Leu	Arg	Cys	Cys	His	Pro	Asn	Val	Leu	Pro	Val
			260					265					270		
Leu	Gly	Phe	Cys	Ala	Ala	Arg	Gln	Phe	His	Ser	Phe	Ile	Tyr	Pro	Tyr
	275						280					285			
Met	Ala	Asn	Gly	Ser	Leu	Gln	Asp	Arg	Leu	Gln	Gly	Gln	Gly	Gly	Ser
290						295					300				
Asp	Pro	Leu	Pro	Trp	Pro	Gln	Arg	Val	Ser	Ile	Cys	Ser	Gly	Leu	Leu
305					310					315					320
Cys	Ala	Val	Glu	Tyr	Leu	His	Gly	Leu	Glu	Ile	Ile	His	Ser	Asn	Val

325								330				335			
Lys	Ser	Ser	Asn	Val	Leu	Leu	Asp	Gln	Asn	Leu	Thr	Pro	Lys	Leu	Ala
			340					345					350		
His	Pro	Met	Ala	His	Leu	Cys	Pro	Val	Asn	Lys	Arg	Ser	Lys	Tyr	Thr
		355					360					365			
Met	Met	Lys	Thr	His	Leu	Leu	Arg	Thr	Ser	Ala	Ala	Tyr	Leu	Pro	Glu
	370					375					380				
Asp	Phe	Ile	Arg	Val	Gly	Gln	Val	Thr	Lys	Arg	Val	Asp	Ile	Phe	Ser
385					390					395					400
Cys	Gly	Ile	Val	Leu	Ala	Glu	Val	Leu	Thr	Gly	Ile	Pro	Ala	Met	Asp
				405					410					415	
Asn	Asn	Arg	Ser	Pro	Val	Tyr	Leu	Lys	Asp	Leu	Leu	Leu	Ser	Glu	Ile
			420					425					430		
Pro	Ser	Ser	Thr	Ala	Ser	Leu	Cys	Ser	Arg	Lys	Thr	Gly	Val	Glu	Asn
		435					440					445			
Val	Met	Ala	Lys	Glu	Ile	Cys	Gln	Lys	Tyr	Leu	Glu	Lys	Gly	Ala	Gly
	450					455					460				
Arg	Leu	Pro	Glu	Asp	Cys	Ala	Glu	Ala	Leu	Ala	Thr	Ala	Ala	Cys	Leu
465					470					475					480
Cys	Leu	Arg	Arg	Arg	Asn	Thr	Ser	Leu	Gln	Glu	Val	Cys	Gly	Ser	Val
				485					490					495	
Ala	Ala	Val	Glu	Glu	Arg	Leu	Arg	Gly	Arg	Glu	Thr	Leu	Leu	Pro	Trp
			500					505						510	
Ser	Gly	Leu	Ser	Glu	Gly	Thr	Gly	Ser	Ser	Ser	Asn	Thr	Pro	Glu	Glu
		515					520					525			
Thr	Asp	Asp	Val	Asp	Asn	Ser	Ser	Leu	Asp	Ala	Ser	Ser	Ser	Met	Ser
	530					535					540				
Val	Ala	Pro	Trp	Ala	Gly	Ala	Ala	Thr	Pro	Leu	Leu	Pro	Thr	Glu	Asn
545					550					555					560
Gly	Glu	Gly	Arg	Leu	Arg	Val	Ile	Val	Gly	Arg	Glu	Ala	Asp	Ser	Ser
				565					570					575	
Ser	Glu	Ala	Cys	Val	Gly	Leu	Glu	Pro	Pro	Gln	Asp	Val	Thr	Glu	Thr
			580					585					590		
Ser	Trp	Gln	Ile	Glu	Ile	Asn	Glu	Ala	Lys	Arg	Lys	Leu	Met	Glu	Asn
		595					600					605			
Ile	Leu	Leu	Tyr	Lys	Glu	Glu	Lys	Val	Asp	Ser	Ile	Glu	Leu	Phe	Gly
	610					615					620				
Pro															
625															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 712 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Gly	Gly	Pro	Gly	Pro	Gly	Glu	Pro	Ala	Ala	Pro	Gly	Ala	Gln	1	5	10	15
His	Phe	Leu	Tyr	Glu	Val	Pro	Pro	Trp	Val	Met	Cys	Arg	Phe	Tyr	Lys	20	25	30	
Val	Met	Asp	Ala	Leu	Glu	Pro	Ala	Asp	Trp	Cys	Gln	Phe	Ala	Ala	Leu	35	40	45	
Ile	Val	Arg	Asp	Gln	Thr	Glu	Leu	Arg	Leu	Cys	Glu	Arg	Ser	Gly	Gln	50	55	60	
Arg	Thr	Ala	Ser	Val	Leu	Trp	Pro	Trp	Ile	Asn	Arg	Asn	Ala	Arg	Val	65	70	75	80
Ala	Asp	Leu	Val	His	Ile	Leu	Thr	His	Leu	Gln	Leu	Leu	Arg	Ala	Arg	85	90	95	
Asp	Ile	Ile	Thr	Ala	Trp	His	Pro	Pro	Ala	Pro	Leu	Pro	Ser	Pro	Gly	100	105	110	
Thr	Thr	Ala	Pro	Arg	Pro	Ser	Ser	Ile	Pro	Ala	Pro	Ala	Glu	Ala	Glu	115	120	125	
Ala	Trp	Ser	Pro	Arg	Lys	Leu	Pro	Ser	Ser	Ala	Ser	Thr	Phe	Leu	Ser	130	135	140	
Pro	Ala	Phe	Pro	Gly	Ser	Gln	Thr	His	Ser	Gly	Pro	Glu	Leu	Gly	Leu	145	150	155	160
Val	Pro	Ser	Pro	Ala	Ser	Leu	Trp	Pro	Pro	Pro	Pro	Ser	Pro	Ala	Pro	165	170	175	
Ser	Ser	Thr	Lys	Pro	Gly	Pro	Glu	Ser	Ser	Val	Ser	Leu	Leu	Gln	Gly	180	185	190	
Ala	Arg	Pro	Ser	Pro	Phe	Cys	Trp	Pro	Leu	Cys	Glu	Ile	Ser	Arg	Gly	195	200	205	
Thr	His	Asn	Phe	Ser	Glu	Glu	Leu	Lys	Ile	Gly	Glu	Gly	Gly	Phe	Gly	210	215	220	
Cys	Val	Tyr	Arg	Ala	Val	Met	Arg	Asn	Thr	Val	Tyr	Ala	Val	Lys	Arg	225	230	235	240
Leu	Lys	Glu	Asn	Ala	Asp	Leu	Glu	Trp	Thr	Ala	Val	Lys	Gln	Ser	Phe	245	250	255	
Leu	Thr	Glu	Val	Glu	Gln	Leu	Ser	Arg	Phe	Arg	His	Pro	Asn	Ile	Val	260	265	270	
Asp	Phe	Ala	Gly	Tyr	Cys	Ala	Gln	Asn	Gly	Phe	Tyr	Cys	Leu	Val	Tyr	275	280	285	

Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr
 290 295 300
 Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu
 305 310 315 320
 Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu
 325 330 335
 Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu
 340 345 350
 Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala
 355 360 365
 Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val
 370 375 380
 Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg
 385 390 395 400
 Leu Ala Val Asp Thr Asp Thr Phe Ser Phe Gly Val Val Val Leu Glu
 405 410 415
 Thr Leu Ala Gly Gln Arg Ala Val Lys Thr His Gly Ala Arg Thr Lys
 420 425 430
 Tyr Leu Lys Asp Leu Val Glu Glu Glu Ala Glu Glu Ala Gly Val Ala
 435 440 445
 Leu Arg Ser Thr Gln Ser Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala
 450 455 460
 Trp Ala Ala Pro Ile Ala Met Gln Ile Tyr Lys Lys His Leu Asp Pro
 465 470 475 480
 Arg Pro Gly Pro Cys Pro Pro Glu Leu Gly Leu Gly Leu Gly Gln Leu
 485 490 495
 Ala Cys Cys Cys Leu His Arg Arg Ala Lys Arg Arg Pro Pro Met Thr
 500 505 510
 Gln Val Tyr Glu Arg Leu Glu Lys Leu Gln Ala Val Val Ala Gly Val
 515 520 525
 Pro Gly His Leu Glu Ala Ala Ser Cys Ile Pro Pro Ser Pro Gln Glu
 530 535 540
 Asn Ser Tyr Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala Pro
 545 550 555 560
 Trp Gln Pro Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala Glu
 565 570 575
 Gln Leu Gln Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser Leu
 580 585 590
 Gly Gly Leu Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser Cys
 595 600 605
 Pro Leu Asp Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly Asp
 610 615 620
 Thr Ala Gly Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro Thr

625		630		635		640
Ala Val Glu Gly	Leu Ala Leu Gly	Ser Ser Ala Ser Ser Ser Ser	Glu			
	645	650	655			
Pro Pro Gln Ile Ile Ile Asn Pro	Ala Arg Gln Lys Met Val Gln Lys					
	660	665	670			
Leu Ala Leu Tyr Glu Asp Gly	Ala Leu Asp Ser Leu Gln Leu Leu Ser					
	675	680	685			
Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro						
	690	695	700			
Glu Glu Ser Asp Glu Phe Gln Ser						
705	710					

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 501 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Gly Val Gln Thr Ala Glu Ala Glu Ala Gln Ala Gln Asn Gln	
1 5 10 15	
Ala Asn Gly Asn Arg Thr Arg Ser Arg Ser His Leu Asp Asn Thr Met	
20 25 30	
Ala Ile Arg Leu Leu Pro Leu Pro Val Arg Ala Gln Leu Cys Ala His	
35 40 45	
Leu Asp Ala Leu Asp Val Trp Gln Gln Leu Ala Thr Ala Val Lys Leu	
50 55 60	
Tyr Pro Asp Gln Val Glu Gln Ile Ser Ser Gln Lys Gln Arg Gly Arg	
65 70 75 80	
Ser Ala Ser Asn Glu Phe Leu Asn Ile Trp Gly Gly Gln Tyr Asn His	
85 90 95	
Thr Val Gln Thr Leu Phe Ala Leu Phe Lys Lys Leu Lys Leu His Asn	
100 105 110	
Ala Met Arg Leu Ile Lys Asp Tyr Val Ser Glu Asp Leu His Lys Tyr	
115 120 125	
Ile Pro Arg Ser Val Pro Thr Ile Ser Glu Leu Arg Ala Ala Pro Asp	
130 135 140	
Ser Ser Ala Lys Val Asn Asn Gly Pro Pro Phe Pro Ser Ser Ser Gly	
145 150 155 160	
Val Ser Asn Ser Asn Asn Asn Arg Thr Ser Thr Thr Ala Thr Glu Glu	
165 170 175	

Ile	Pro	Ser	Leu	Glu	Ser	Leu	Gly	Asn	Ile	His	Ile	Ser	Thr	Val	Gln	
			180					185					190			
Arg	Ala	Ala	Glu	Ser	Leu	Leu	Glu	Ile	Asp	Tyr	Ala	Glu	Leu	Glu	Asn	
		195					200					205				
Ala	Thr	Asp	Gly	Trp	Ser	Pro	Asp	Asn	Arg	Leu	Gly	Gln	Gly	Gly	Phe	
	210					215					220					
Gly	Asp	Val	Tyr	Arg	Gly	Lys	Trp	Lys	Gln	Leu	Asp	Val	Ala	Ile	Lys	
225					230					235					240	
Val	Met	Asn	Tyr	Arg	Ser	Pro	Asn	Ile	Asp	Gln	Lys	Met	Val	Glu	Leu	
			245						250					255		
Gln	Gln	Ser	Tyr	Asn	Glu	Leu	Lys	Tyr	Leu	Asn	Ser	Ile	Arg	His	Asp	
			260					265					270			
Asn	Ile	Leu	Ala	Leu	Tyr	Gly	Tyr	Ser	Ile	Lys	Gly	Gly	Lys	Pro	Cys	
		275					280					285				
Leu	Val	Tyr	Gln	Leu	Met	Lys	Gly	Gly	Ser	Leu	Glu	Ala	Arg	Leu	Arg	
	290					295					300					
Ala	His	Lys	Ala	Gln	Asn	Pro	Leu	Pro	Ala	Leu	Thr	Trp	Gln	Gln	Arg	
305					310					315					320	
Phe	Ser	Ile	Ser	Leu	Gly	Thr	Ala	Arg	Gly	Ile	Tyr	Phe	Leu	His	Thr	
			325						330					335		
Ala	Arg	Gly	Thr	Pro	Leu	Ile	His	Gly	Asp	Ile	Lys	Pro	Ala	Asn	Ile	
			340					345					350			
Leu	Leu	Asp	Gln	Cys	Leu	Gln	Pro	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Val	
		355					360					365				
Arg	Glu	Gly	Pro	Lys	Ser	Leu	Asp	Ala	Val	Val	Glu	Val	Asn	Lys	Val	
	370					375					380					
Phe	Gly	Thr	Lys	Ile	Tyr	Leu	Pro	Pro	Glu	Phe	Arg	Asn	Phe	Arg	Gln	
385					390					395					400	
Leu	Ser	Thr	Gly	Val	Asp	Val	Tyr	Ser	Phe	Gly	Ile	Val	Leu	Leu	Glu	
			405						410					415		
Val	Phe	Thr	Gly	Arg	Gln	Val	Thr	Asp	Arg	Val	Pro	Glu	Asn	Glu	Thr	
			420					425					430			
Lys	Lys	Asn	Leu	Leu	Asp	Tyr	Val	Lys	Gln	Gln	Trp	Arg	Gln	Asn	Arg	
		435					440					445				
Met	Glu	Leu	Leu	Glu	Lys	His	Leu	Ala	Ala	Pro	Met	Gly	Lys	Glu	Leu	
	450					455					460					
Asp	Met	Cys	Met	Cys	Ala	Ile	Glu	Ala	Gly	Leu	His	Cys	Thr	Ala	Leu	
465					470					475					480	
Asp	Pro	Gln	Asp	Arg	Pro	Ser	Met	Asn	Ala	Val	Leu	Lys	Arg	Phe	Glu	
			485						490					495		
Pro	Phe	Val	Thr	Asp												
			500													

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACGAGCA CCTTTCAGG CCCAGGGTCC TNTCCAGCCA GAGCCCACCA GCCGGCCTTT	60
CTCCAGCCTC CTGAAGAAGA TNNCCCTCAT TCCTTGAGAA GCGACCTCCC CACTTCGTCT	120
GNTTCAAAGG ACTTCAGCAC CTCCATTCCT AAGCAGGAAA AACTTTTGAG CTTGGCTGGA	180
GACAGATGNT TCTGGTGTGA GGCAGACGTG GTCCAGTCAA CCGATGACTT GANTNNTAAC	240
CGCAGAATCA GNCAGGGGAC CTTTG	265

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACGTCAAGA GCTCTAATNT CTTGCTGGAC CAAAATCTNA CCCCCAACT TGCTCACCCA	60
ATGGCTCATC TGTGTCCTGT NAACAAAAGG TCAAAATACA CCATGATGAT GACTCACCTG	120
GCTCCGGAAC GTCAGCCGCG TATCTCCCAG NGGATTTNAT CCGGAGTGGG GCAGCTGAAC	180
AAAGCGAGTG GACATCTTCA GCTGTGGAAT AGTGTTGGAC GAGGTNCTCA CGGGGNATCC	240
CTGTCAATGG GTTAACANCC GAAGCCCGGT TTACCTGAAG GNACTTAATT NCTC	294

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CNCTAATGTN TTNCTGGACC AAAATNTCAC CCCCAAAC TT CTCACCCAA TGGCTCATCT	60
NTTTCCTGTC AACAAAAGGT CAAAATACAC CATGATGAAG ACTCACCTGC TCCGGACGTC	120
AGCCGCGTAT CTGCCCAGAG GATTTCATCC GNGTGGGGCA GCTGACAAAG CGAGTGGACA	180
TCTTCAGCTG TGGAAATAGTA AGAGTGTCC T GCTCTGCGTA GAAGTGGGGC CCACCTTGAA	240
TTTGTCCCTT CCACGGTTCC TTTGTNAATC ACAGGATACG GTAGAGNCAC ACAGACAGGT	300
TCCNNCAAGT NACAACAGGG GCTGTACAAA	330

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCGGCAN AGNATGGAGT TCGCCTCCTA CGTGATCACA GACCTGACCC AGCTGCGGAA	60
GATCAAGTCC ATGGAGCGGG TGCAGGGTGT GAGCATCACG CGGGGNGCTG CTGTGGTGGT	120
GGGGCATGCG GCAGGCCACC GTCCAGCAAC TTGTGGGACC TCCTGTGCCG CCTGGGAGCT	180
CTACCGGGNT GCCCAGATCA TCCTGGAAC TGTGGACACA AGACTTCTCA CATCTGAGAT	240
GGCCCCCTCTG TGCCCCCTACA TGCACATTGG CAGACAGCAA GAAGGGAAAA AGAGGGAAAA	300
AGGGAAACCG GCTNCTGGAA ATCAGGTGTN CCCATTTC A GNCTTTCCCT GAATTCTNTG	360
GAAGGCCAGA AAAAGCCTTT TGGCAAGGTT TTTGTTAAGN AAAGGNTNNA GGTGTAACCA	420
GGAAGAGGGG GCAGNCTTTN AAGGNNTGGG CCACTTTT TN CAGGGCCCCA GGGGTCCTTT	480
TNCAGCCCGN GGNCCAACC	499

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGCACNAGG NGGGTCATCG TGGGAAGGGA AGGCTGACTC CTCCTCTGAA GGACTGTTTT	60
GGANCTAGAG CGTCCCCAGG NTGTTACAGA AACTTCGTGG NNAAATTGAG AATCAATGAG	120

GGCAAAAGGA AACTGATGGN GAATATTCTG CTCTACAANG AGGGAGAAAG TGGNCAGNAT	180
TGAGCTNTTT GGCCCTAAT GACCGGAACA GAGCTGAGGN NCCTTGTCCCT CAGTTGGAAA	240
GATGAGCATC AGATCAAGAA AAAGGTCTGA GGTAGANTNC AAGATCTGNC ANGNAACANA	300
CANCANGACA TCTGCTGTCC TNGGTGGGGG GGAAACTTAT TTACTGGAAT GAGTTTGGAG	360
AGAAAGGCCC TCAANATTTT GGTGGCACAA ANATCCATGA AGGNTATTCG ATN	413

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGAGAAGCCG CAGCCCGCAG TGTCCGACCC AGTCGTCCCG CGCCGGAGCC GGCCCCGTAG	60
CGTGCCATGG CCTGCTACAT CTACCAGCTG CCCTCCTGGG TGCTGGACGA CCTGTGCCGC	120
AACATGGACG CGCTCAGGAG TGGGACTGGA TGGAGTTCGG TGAGTGCGGC CCGGGGAGGG	180
GAGGGGACCA GGGCGACCGG AGCCCCCAGC GATCCCGCCT GGAGCGGCCG CCAAGCTCCC	240
TCGGGCACCC GGGTTCAGCG GGTCCCGATC CGAGGGCGTG CGAGCTGAGC CTCCTGGAC	300
CGGGTTCCGC CGCGGACCTT CGGCCTGTTC ACCTGAAGGT GCCGGTGGTC TCTGAGGACG	360
TCTGTTTCGAC GAGCCAGGGG CCGCCGCCAC TGCGCTCTGA GTCCAGAGAA CGGTGGGTAC	420
GGGGGCCCTC CTGTCAGCGC TGCTGGCTCG GTGACGTCCC CAGGTGGCCT CTCATCCAGC	480
CCACAACAGC CTGCAAAGTG CGAGCCTCGA CCCTGTAGGG ACCCACGGTG CTGTCACTTC	540
TTGGGGGTGT GTGTGTGTGT GTGTGTGTGG TGTGTTTAGT TTTAGTGTAT ATTAGAAGGA	600
TCTATGATTT AACATATATA TATATATTGA AACAGAGCAA GATTCTGTCT CAAAAAAAAA	660
AAAAA	665

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGGAACTG ATGGNGAATA TTCTGCTCTA CAAAGAGGNA AAAAGTGGAC AGCATTGAGC	60
TCTTTGGCCC CTGATGACCG GAACACAGCT GAGGACCCTT GTCCTCAGTT GGAAAGATGA	120
GCATCAGATC AAGAAAAAGG TCTGAGGCAG AATCCAAGAT CTGCCAGGAA ACACACAACA	180
AAACATCTGC TGTCTTGGGT GGGAGGGAAA CTTCAATTCA CTGGAATGAG TTGGGAGAGA	240
AAGGCCCTCA GCTTTTNGGG ANACAAAATT CCNTGAGGTT TTTCCCTTCN TGGTTTNTAA	300
GTAAGGGCAG GGTAAAGGG TTTAGGA	327

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTATTAAGG CCAGAGAGTG CAACTCACAC GGATGGAAAC TGCTCAGGAG CGTGATGGGC	60
CCCACCCAAG GAGGGCCTGG AGTTACTCAC AGTTCAGGAT GATCTGGGCA GCCCGGTAGA	120
GCTCCAGGCG GCACAGGAGG TCCACAAGTT GCTGGACGGT GGCCTGCCGC ATGCCCCACC	180
ACCACAGCAG CTCCCGCGTG ATGCTCACAC CCTGCACCCG CTCCATGGAC TTGATCTTCC	240
GCAGCTGGGT CAGGTCTGTG ATCACGTAGG AGGCTGGAAG GGACAGAGAG AACTCTGCTT	300
AGAGTCAGAG AGGCAGTCCC TCTAGGACAG GTCCCCACAC TAAGCCCCTA GCTTGGGTTT	360
TTCCAGGACA TCCTCCCCAA CCAACCGCCT CCACACTGGA AACACCACCA TTAAGCTGAG	420
GTCCACAGGT GGCCAAGTTA CAACGCTGAC TCTGCTGGGC ACCCATGGGG TCCAGTACA	479